



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/039,177B
Source: 1647
Date Processed by STIC: 2/14/2001

RECEIVED

MAR 01 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

1647

RAW SEQUENCE LISTING DATE: 02/14/2001
 PATENT APPLICATION: US/09/039,177B TIME: 17:37:04

**Does Not Comply
 Corrected Diskette Needed**

Input Set : A:\LUD-5539 SEQUENCE LISTING.txt
 Output Set: N:\CRF3\02142001\I039177B.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
 5 (i) APPLICANT: Kohei MIYAZONO; Takeshe IMAMURA; Peter DEN DIJKE
 7 (ii) TITLE OF INVENTION: ISOLATED ALK-1 PROTEIN, NUCLEIC ACIDS ENCODING
 8 IT, AND USES THEREOF
 10 (iii) NUMBER OF SEQUENCES: 46
 12 (iv) CORRESPONDENCE ADDRESS:
 13 (A) ADDRESSEE: Fulbright & Jaworski L.L.P.
 14 (B) STREET: 666 Fifth Avenue
 15 (C) CITY: New York City
 16 (D) STATE: New York
 17 (E) COUNTRY: USA
 18 (F) ZIP: 10103
 20 (v) COMPUTER READABLE FORM:
 21 (A) MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
 22 (B) COMPUTER: IBM PS/2
 23 (C) OPERATING SYSTEM: PC-DOS
 24 (D) SOFTWARE: Wordperfect
 26 (vi) CURRENT APPLICATION DATA:
 C--> 27 (A) APPLICATION NUMBER: US/09/039,177B
 C--> 28 (B) FILING DATE: 13-Mar-1998
 29 (C) CLASSIFICATION: 435
 59 (vii) PRIOR APPLICATION DATA:
 32 (A) APPLICATION NUMBER: PCT/GB93/02367
 33 (B) FILING DATE: November 17, 1993
 36 (A) APPLICATION NUMBER: GB 9224057.1
 37 (B) FILING DATE: November 17, 1992
 40 (A) APPLICATION NUMBER: GB 9304677.9
 41 (B) FILING DATE: March 8, 1993
 44 (A) APPLICATION NUMBER: GB 9304680.3
 45 (B) FILING DATE: March 8, 1993
 48 (A) APPLICATION NUMBER: 9311047.6
 49 (B) FILING DATE: May 28, 1993
 52 (A) APPLICATION NUMBER: 9313763.6
 53 (B) FILING DATE: July 2, 1993
 56 (A) APPLICATION NUMBER: 9136099.2
 57 (B) FILING DATE: August 3, 1993
 60 (A) APPLICATION NUMBER: 321344.5
 61 (B) FILING DATE: October 15, 1993
 63 (viii) ATTORNEY/AGENT INFORMATION:
 64 (A) NAME: Mary Anne Schofield
 65 (B) REGISTRATION NUMBER: 36,669
 66 (C) REFERENCE/DOCKET NUMBER: LUD 5539 CIP - JEL/MAS
 68 (ix) TELECOMMUNICATION INFORMATION:
 69 (A) TELEPHONE: (202) 662-0200
 70 (B) TELEFAX: (202) 662-4643

RAW SEQUENCE LISTING DATE: 02/14/2001
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Input Set : A:\LUD-5539 SEQUENCE LISTING.txt
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ERRORED SEQUENCES

2641 (2) INFORMATION FOR SEQ ID NO: 32:
 2642 (i) SEQUENCE CHARACTERISTICS:
 2643 (A) LENGTH: 175 amino acids
 2644 (B) TYPE: amino acid
 2645 (D) TOPOLOGY: linear
 2647 (ii) MOLECULE TYPE: peptide
 2649 (vi) ORIGINAL SOURCE:
 2650 (A) ORGANISM: Mouse
 2652 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:
 2654 Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys Ala
 2655 5 10 15
 2656 Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Ile Gln Asp
 2657 20 25 30
 2658 Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser Leu Pro Gly Met
 2659 35 40 45
 2660 Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu Lys Arg Gly Thr
 2661 50 55 60
 2662 Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe His Glu Lys Gly
 2663 65 70 75 80
 2664 Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser Trp Asn Glu Leu
 2665 85 90 95
 2666 Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His Glu
 2667 100 105 110
 2668 Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala Ile Ser His Arg
 2669 115 120 125
 2670 Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala Cys
 2671 130 135 140
 2672 Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala Gly Lys Ser Ala
 2673 145 150 155 160
 2674 Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro
 E--> 2675 165 170 175

(see item 4 on
 Error Summary Sheet)

misaligned amino
 acid numbering

165

170

2717 (2) INFORMATION FOR SEQ ID NO: 34:
 2718 (i) SEQUENCE CHARACTERISTICS:
 2719 (A) LENGTH: 513 amino acids
 2720 (B) TY7PE amino acid *TYPE*
 2721 (D) TOPOLOGY: linear
 2723 (ii) MOLECULE TYPE: peptide
 2725 (vi) ORIGINAL SOURCE:
 2726 (A) ORGANISM: MOUSE
 2728 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:
 2730 SEQ ID NO: 34 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

E--> 2731 ~~Mouse ActR II~~ *delete this*

E--> 2733 Met Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu Ile Ser Cys
 2734 5 10 15
 2735 Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu Cys Leu Phe
 2736 20 25 30
 2737 Phe Asn Ala Asn Trp Glu Lys Asp Arg Thr Asn Gln Thr Gly Val Glu
 2738 35 40 45

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Input Set : A:\LUD-5539 SEQUENCE LISTING.txt

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```

2739 Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe Ala Thr Trp
2740      50                      55                      60
2741 Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly Cys Trp Leu
2742 65      -                      70                      75                      80
2743 Asp Asp Ile Asn Cys Tyr Asp Arg Thr Asp Cys Val Glu Lys Lys Asp
2744      85                      90                      95
2745 Ser Pro Glu Val Tyr Phe Cys Cys Cys Glu Gly Asn Met Cys Asn Glu
2746      100                     105                     110
2747 Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro Thr Ser Asn
2748      115                     120                     125
2749 Pro Val Thr Pro Lys Pro Pro Tyr Tyr Asn Ile Leu Leu Tyr Ser Leu
2750      130                     135                     140
2751 Val Pro Leu Met Leu Ile Ala Gly Ile Val Ile Cys Ala Phe Trp Val
2752 145      150                     155                     160
2753 Tyr Arg His His Lys Met Ala Tyr Pro Pro Val Leu Val Pro Thr Gln
2754      165                     170                     175
2755 Asp Pro Gly Pro Pro Pro Pro Ser Pro Leu Leu Gly Leu Lys Pro Leu
2756      180                     185                     190
2757 Gln Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys
2758      195                     200                     205
2759 Ala Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Ile Gln
2760      210                     215                     220
2761 Asp Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser Leu Pro Gly
2762 225      230                     235                     240
2763 Met Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu Lys Arg Gly
2764      245                     250                     255
2765 Thr Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe His Glu Lys
2766      260                     265                     270
2767 Gly Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser Trp Asn Glu
2768      275                     280                     285
2769 Leu Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His
2770      290                     295                     300
2771 Glu Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala Ile Ser His
2772 305      310                     315                     320
2773 Arg Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala
2774      325                     330                     335
2775 Cys Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala Gly Lys Ser
2776      340                     345                     350
2777 Ala Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro
2778      355                     360                     365
2779 Glu Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala Phe Leu Arg
2780      370                     375                     380
2781 Ile Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu Ala Ser Arg
2782 385      390                     395                     400
2783 Cys Thr Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu Pro Phe Glu
2784      405                     410                     415
2785 Glu Glu Ile Gly Gln His Pro Ser Leu Glu Asp Met Gln Glu Val Val
2786      420                     425                     430
2787 Val His Lys Lys Lys Arg Pro Val Leu Arg Asp Tyr Trp Gln Lys His

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2788 435 440 445
 2789 Ala Gly Met Ala Met Leu Cys Glu Thr Ile Glu Glu Cys Trp Asp His
 2790 450 455 460
 2791 Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Gly Glu Arg Ile Thr
 2792 465 470 475 480
 2793 Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu Asp Ile Val Thr
 2794 485 490 495
 2795 Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro Lys Glu Ser Ser
 2796 500 505 510
 E--> 2797 Leu
 2800 (2) INFORMATION FOR SEQ ID NO: 35:
 2801 (i) SEQUENCE CHARACTERISTICS:
 2802 (A) LENGTH: 536 amino acids
 2803 (B) TYPE: amino acid
 2804 (D) TOPOLOGY: linear
 2806 (ii) MOLECULE TYPE: peptide
 2808 (vi) ORIGINAL SOURCE:
 2809 (A) ORGANISM: MOUSE
 2811 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:
 E--> 2811 ACTR- IIB *delete*
 E--> 2815 Met Thr Ala Pro Trp Ala Ala Leu Ala Leu Leu Trp Gly Ser Leu Cys
 2816 5 10 15
 2818 Ala Gly Ser Gly Arg Gly Glu Ala Glu Thr Arg Glu Cys Ile Tyr Tyr
 2819 20 25 30
 2820 Asn Ala Asn Trp Glu Leu Glu Arg Thr Asn Gln Ser Gly Leu Glu Arg
 2821 35 40 45
 2822 Cys Glu Gly Glu Gln Asp Lys Arg Leu His Cys Tyr Ala Ser Trp Arg
 2823 50 55 60
 2824 Asn Ser Ser Gly Thr Ile Glu Leu Val Lys Lys Gly Cys Trp Leu Asp
 2825 65 70 75 80
 2826 Asp Phe Asn Cys Tyr Asp Arg Gln Glu Cys Val Ala Thr Glu Glu Asn
 2827 85 90 95
 2828 Pro Gln Val Tyr Phe Cys Cys Cys Glu Gly Asn Phe Cys Asn Glu Arg
 2829 100 105 110
 2830 Phe Thr His Leu Pro Glu Pro Gly Gly Pro Glu Val Thr Tyr Glu Pro
 2831 115 120 125
 2832 Pro Pro Thr Ala Pro Thr Leu Leu Thr Val Leu Ala Tyr Ser Leu Leu
 2833 130 135 140
 2834 Pro Ile Gly Gly Leu Ser Leu Ile Val Leu Leu Ala Phe Trp Met Tyr
 2835 145 150 155 160
 2836 Arg His Arg Lys Pro Pro Tyr Gly His Val Asp Ile His Glu Val Arg
 2837 165 170 175
 2838 Gln Cys Gln Arg Trp Ala Gly Arg Arg Asp Gly Cys Ala Asp Ser Phe
 2839 180 185 190
 2840 Lys Pro Leu Pro Phe Gln Asp Pro Gly Pro Pro Pro Pro Ser Pro Leu
 2841 195 200 205
 2842 Val Gly Leu Lys Pro Leu Gln Leu Leu Glu Ile Lys Ala Arg Gly Arg
 2843 210 215 220
 2844 Phe Gly Cys Val Trp Lys Ala Gln Leu Met Asn Asp Phe Val Ala Val

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Input Set : A:\LUD-5539 SEQUENCE LISTING.txt

Output Set: N:\CRF3\02142001\I039177B.raw

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2845 225          230          235          240
2846 Lys Ile Phe Pro Leu Gln Asp Lys Gln Ser Trp Gln Ser Glu Arg Glu
2847          245          250          255
2848 Ile Phe Ser Thr Pro Gly Met Lys His Glu Asn Leu Leu Gln Phe Ile
2849          260          265          270
2850 Ala Ala Glu Lys Arg Gly Ser Asn Leu Glu Val Glu Leu Trp Leu Ile
2851          275          280          285
2852 Thr Ala Phe His Asp Lys Gly Ser Leu Thr Asp Tyr Leu Lys Gly Asn
2853          290          295          300
2854 Ile Ile Thr Trp Asn Glu Leu Cys His Val Ala Glu Thr Met Ser Arg
2855 305          310          315          320
2856 Gly Leu Ser Tyr Leu His Glu Asp Val Pro Trp Cys Arg Gly Glu Gly
2857          325          330          335
2858 His Lys Pro Ser Ile Ala His Arg Asp Phe Lys Ser Lys Asn Val Leu
2859          340          345          350
2860 Leu Lys Ser Asp Leu Thr Ala Val Leu Ala Asp Phe Gly Leu Ala Val
2861          355          360          365
2862 Arg Phe Glu Pro Gly Lys Pro Pro Gly Asp Thr His Gly Gln Val Gly
2863          370          375          380
2864 Thr Arg Arg Tyr Met Ala Pro Glu Val Leu Glu Gly Ala Ile Asn Phe
2865 385          390          395          400
2866 Gln Arg Asp Ala Phe Leu Arg Ile Asp Met Tyr Ala Met Gly Leu Val
2867          405          410          415
2868 Leu Trp Glu Leu Val Ser Arg Cys Lys Ala Ala Asp Gly Pro Val Asp
2869          420          425          430
2870 Glu Tyr Met Leu Pro Phe Glu Glu Ile Gly Gln His Pro Ser Leu
2871          435          440          445
2872 Glu Glu Leu Gln Glu Val Val His Lys Lys Met Arg Pro Thr Ile
2873          450          455          460
2874 Lys Asp His Trp Leu Lys His Pro Gly Leu Ala Gln Leu Cys Val Thr
2875 465          470          475          480
2876 Ile Glu Glu Cys Trp Asp His Asp Ala Glu Ala Arg Leu Ser Ala Gly
2877          485          490          495
2878 Cys Val Glu Glu Arg Val Ser Leu Ile Arg Arg Ser Val Asn Gly Thr
2879          500          505          510
2880 Thr Ser Asp Cys Leu Val Ser Leu Val Thr Ser Val Thr Asn Val Asp
E--> 2881          515          520          525          530
2882 Leu Leu Pro Lys Glu Ser Ser Ile
E--> 2883          530          535          540          545
3075 (2) INFORMATION FOR SEQ ID NO: 38:
3076 (i) SEQUENCE CHARACTERISTICS:
3077 (A) LENGTH: 6 amino acids
3078 (B) TYPE: amino acid
3079 (D) TOPOLOGY: linear
3081 (ii) MOLECULE TYPE: peptide
3083 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:
3085 Asp Leu Lys Pro Glu Asn
E--> 3086          5          535
3092 (2) INFORMATION FOR SEQ ID NO: 39:

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misaligned nos.~~520~~~~525~~

RAW SEQUENCE LISTING DATE: 02/14/2001
PATENT APPLICATION: US/09/039,177B TIME: 17:37:04

Input Set : A:\LUD-5539 SEQUENCE LISTING.txt
Output Set: N:\CRF3\02142001\I039177B.raw

3093 (i) SEQUENCE CHARACTERISTICS:
3094 (A) LENGTH: 6 amino acids
3095 (B) TYPE: amino acid
3096 (D) TOPOLOGY: linear
3098 (ii) MOLECULE TYPE: peptide
3100 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:
3102 Asp Leu Ala Ala Arg Asn
E--> 3103 S 5
3106 (2) INFORMATION FOR SEQ ID NO: 40:
3107 (i) SEQUENCE CHARACTERISTICS:
3108 (A) LENGTH: 6 amino acids
3109 (B) TYPE: amino acid
3110 (D) TOPOLOGY: linear
3112 (ii) MOLECULE TYPE: peptide
3114 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:
3116 Asp Ile Lys Ser Lys Asn
E--> 3117 S 5
3120 (2) INFORMATION FOR SEQ ID NO: 41:
3121 (i) SEQUENCE CHARACTERISTICS:
3122 (A) LENGTH: 6 amino acids
3123 (B) TYPE: amino acid
3124 (D) TOPOLOGY: linear
3126 (ii) MOLECULE TYPE: peptide
3128 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:
3130 Asp Phe Lys Ser Lys Asn
E--> 3131 S 5
3134 (2) INFORMATION FOR SEQ ID NO: 42:
3135 (i) SEQUENCE CHARACTERISTICS:
3136 (A) LENGTH: 6 amino acids
3137 (B) TYPE: amino acid
3138 (D) TOPOLOGY: linear
3140 (ii) MOLECULE TYPE: peptide
3142 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:
3144 Asp Leu Lys Ser Ser Asn
E--> 3145 S 5
3148 (2) INFORMATION FOR SEQ ID NO: 43:
3149 (i) SEQUENCE CHARACTERISTICS:
3150 (A) LENGTH: 6 amino acids
3151 (B) TYPE: amino acid
3152 (D) TOPOLOGY: linear
3154 (ii) MOLECULE TYPE: peptide
3156 (ix) FEATURE:
3157 (D) OTHER INFORMATION: First Xaa is Thr or Ser;
3158 fourth Xaa is Tyr or Phe; Each other Xaa
3159 may be any amino acid
3161 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:
W--> 3163 Gly Xaa Xaa Xaa Xaa Xaa
E--> 3164 S 5
3167 (2) INFORMATION FOR SEQ ID NO: 44:

misaligned nos.

RAW SEQUENCE LISTING

DATE: 02/14/2001

PATENT APPLICATION: US/09/039,177B

TIME: 17:37:04

Input Set : A:\LUD-5539 SEQUENCE LISTING.txt

Output Set: N:\CRF3\02142001\I039177B.raw

3168 (i) SEQUENCE CHARACTERISTICS:
3169 (A) LENGTH: 6 amino acids
3170 (B) TYPE: amino acid
3171 (D) TOPOLOGY: linear
3173 (ii) MOLECULE TYPE: peptide *First*
3175 (ix) FEATURE:
3176 (D) OTHER INFORMATION: *Fisrt* Xaa is any amino acid;
3177 second Xaa is Ile or Val;
3178 third Xaa is Lys or Arg;
3179 fourth Xaa is Thr or Met.
3181 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:
W--> 3183 Xaa Pro Xaa Xaa Trp Xaa
E--> 3184 *5*
3187 (2) INFORMATION FOR SEQ ID NO: 45:
3188 (i) SEQUENCE CHARACTERISTICS:
3189 (A) LENGTH: 6 amino acids
3190 (B) TYPE: amino acid
3191 (D) TOPOLOGY: linear
3193 (ii) MOLECULE TYPE: peptide
3195 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:
3197 Gly Thr Arg Arg Tyr Met
E--> 3198 *5*
3200 (2) INFORMATION FOR SEQ ID NO: 46:
3201 (i) SEQUENCE CHARACTERISTICS:
3202 (A) LENGTH: *2* amino acids *mandatory response needed*
3203 (B) TYPE: amino acid
3204 (D) TOPOLOGY: linear
3206 (ii) MOLECULE TYPE: peptide
3208 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:
3210 Gly Thr Ala Arg Tyr Met
E--> 3211 *5* *misaligned nos.*

all next page - more errors

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 669 amino acids

(B) TY7PE amino acid → TYPE

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: C. elegans

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

SEQ ID NO: 37

C. elegans Daf-1: *delete*

VERIFICATION SUMMARY

DATE: 02/14/2001

PATENT APPLICATION: US/09/039,177B

TIME: 17:37:05

Input Set : A:\LUD-5539 SEQUENCE LISTING.txt

Output Set: N:\CRF3\02142001\I039177B.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:85 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:331 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:602 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:887 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1143 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1398 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1640 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1897 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2148 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2391 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2409 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2427 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2445 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2463 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2481 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2499 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:2675 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:32
L:0 M:200 E: Mandatory Header Field missing, Seq 34, [(B) TYPE:] of (2)(i)
L:2731 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:2731 M:330 E: (2) Invalid Amino Acid Designator, 2
L:2733 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:2797 M:203 E: No. of Seq. differs, LENGTH:Input:513 Found:515 SEQ:34
L:2813 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:2813 M:330 E: (2) Invalid Amino Acid Designator, 2
L:2815 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
M:332 Repeated in SeqNo=35
L:2883 M:203 E: No. of Seq. differs, LENGTH:Input:536 Found:538 SEQ:35
L:0 M:200 E: Mandatory Header Field missing, Seq 37, [(B) TYPE:] of (2)(i)
L:3086 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:38
L:3103 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:39
L:3117 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:40
L:3131 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:41
L:3145 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:42
L:3163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:3164 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:43
L:3183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:3184 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:44
L:3198 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:45
L:3211 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:46
L:3211 M:203 E: No. of Seq. differs, LENGTH:Input:0 Found:6 SEQ:46

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/039,177B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☒ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ☐ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ☐ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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